



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/670,756

Source: O1PE

Date Processed by STIC: 10/4/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old 37 CFR) and the revised version of 37 CFR §§1.821 – 1.825 effective October 1, 1995 (new 37 CFR). The Checker Version 3.0 application is based on the World Intellectual Property Organization (WIPO) Standard ST.28.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is 12K compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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Raw Sequence Listing Error Summary

| <u>ERROR DETECTED</u> | <u>SUGGESTED CORRECTION</u> | <u>SERIAL NUMBER:</u> <u>09/670,756</u> |
|---|---|---|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE | | |
| 1 <input type="checkbox"/> Wrapped Nucleic | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". | |
| 2 <input type="checkbox"/> Wrapped Aminos | The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". | |
| 3 <input type="checkbox"/> Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. | |
| 4 <input type="checkbox"/> Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. | |
| 5 <input type="checkbox"/> Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed. | |
| 6 <input type="checkbox"/> Variable Length | Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. | |
| 7 <input type="checkbox"/> PatentIn ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. | |
| 8 <input type="checkbox"/> Skipped Sequences (OLD RULES) | Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES" response to include the skipped sequence(s). | |
| 9 <input type="checkbox"/> Skipped Sequences (NEW RULES) | Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: <210> sequence id number <400> sequence id number 000 | |
| 10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. | |
| 11 <input type="checkbox"/> Use of <213>Organism (NEW RULES) | Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response. Use of <220> to <213> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown". Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec 1 823 of new Rules) | |
| 12 <input type="checkbox"/> Use of <220>Organism (NEW RULES) | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupt file resulting in the loss of all PTO numeric identifiers and responses (as indicated in raw sequence file). Instead, please use "File Manager" or any other means to copy file to floppy disk. | |
| 13 <input type="checkbox"/> PatentIn ver. 2.0 "bug" | | |

O I P E

P. 6

RAW SEQUENCE LISTING DATE: 10/01/2001
PATENT APPLICATION NO. US/09/670,756 TIME: 10:11:51

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Output Set : N:\CRF3\10042000\1670756.raw

Does Not Comply
Correctly Filled Out

RAW SEQUENCE LISTING
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FILING APPLICATION: US/09/670,756
FILED: 12/14/01
TIME: 11:41:56

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 196 Tyr Thr Tyr Pro Val Leu Ile Gln Asp Thr Pro Asn Gln His Val Asp
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 198 Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gln Ile Val Thr Leu
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 206 213 LENGTH 1886
 207 212 TYPE: DNA
 208 213 ORGANISM: *Patellula* sp.
 209 210 FEATURE:
 210 213 NAME/KEY: CDS
 211 212 LOCATION: (300)..(1600)
 212 213 FRAME: 7

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/670,756

Input Set: A:\seqlist.txt
Output Set: N:\CRF3\10042000\I670756.raw

and found to be the most effective technique in this particular application. The approach of the author is to use the available information to determine the best solution, and to make the best use of the available information. The author's approach is to use the available information to determine the best solution, and to make the best use of the available information.

31/6/70, 756

6

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Val Val Leu Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile
20 25 30

Asp Leu Ser Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val
35 40 45

Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
50 55 60

Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
65 70 75 80

Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys (Xaa) Ile Tyr Ala Gln
85 90 95

Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
100 105 110

Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
115 120 125

Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Lys
130 135 140

Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
145 150 155 160

Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
165 170 175

Tyr Thr Tyr Leu Val Leu Lys Glu Asp Thr Ser Arg Gln His Val Asp
180 185 190

Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp
195 200

All item 10
in Env
summary
sheet

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT FILING NUMBER: US/09/670,756

DATE: 10/17/2010
TIME: 10:11:27

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Output Set: N:\CRE3\10042000\1670756.raw

L-111 M-06 W- Current Application Number differs. Replaced Application Number
L-113 M-07 C- Current Filing Date differs. Replaced Current Filing Date
L-381 M-08 W- (16) "h" or "Xaa" used for SEQ ID# 11
L-383 M-08 W- (16) "h" or "Xaa" used for SEQ ID# 13
L-384 M-08 W- Mandatorily Feature missing. 2.1 not found for SEQ ID# 11
L-385 M-08 W- Mandatorily Feature missing. 2.1 not found for SEQ ID# 13
L-386 M-08 W- Mandatorily Feature missing. 2.3 not found for SEQ ID# 11
L-386 M-08 W- (16) "h" or "Xaa" used. Feature required for SEQ ID# 11
L-3928 M-08 W- (16) "h" or "Xaa" used. Feature required for SEQ ID# 13
L-3362 M-258 W- Mandatorily Feature missing. 2.21 not found for SEQ ID# 13
L-3363 M-258 W- Mandatorily Feature missing. 2.22 not found for SEQ ID# 13
L-3364 M-258 W- (16) "h" or "Xaa" used. Feature required for SEQ ID# 13
L-3365 M-258 W- Mandatorily Feature missing. 2.22 not found for SEQ ID# 13
M-840 Repeated in SeqN 143